

SEQUENCE LISTING

<110> Novozymes A/S

<120> Detection system for high expressing recombinant Bacillus

<130> 10355

<160> 11

<170> PatentIn version 3.2

<210> 1

<211> 2349

<212> DNA

<213> Bacillus subtilis

<220>

<221> YkdA_protein

<222> (1000)..(2349)

<223> 1-999 is promoter

<220>

<221> CDS

<222> (1000)..(2349)

<400> 1

tctttcaagg attcatgttt gtttaccaac ctgttctgta agcagttcat attttctcag	60
ggttctttca aatacctcat caaaaacgtc cggcacagag gcgtgtatca cctcagctcc	120
ctctcccggtt attccgcctt tggttgcaac acgttccagc gtctcctoga aagacatatt	180
tttttcgata agcatcttgc cagttccgta tagcgaatga atcagaaaat caaaggcttc	240
ttctttggac aggctgctgt ttctgacggc agacagtgcc agttcttcaa agattgcagc	300
tatgaatccc ggtgcccagc tcgttaaatt gctggccaca tctaaattcg attctttgat	360
ttcccgtaca cggctgaaaa ccgataacaa ttcattcaga cgttcttttt tctctgcagc	420
cagtgtttca ctgtgaacga caagtgagat gccggcttct gcttcggacg taatggcagg	480
aataacacgt gagataccgg cttctgtttc tgcctccaaa agacgcagcg gcacaccggc	540
agctatggat acgatgtgag tatttctgtt cacatacggg tacagacggc gcattgtttc	600
gatgacatgg agtggcggga cgcataatcaa aatcaattgg cacgtatttg cccaattctc	660
caacggatca gccgatacgt ttggataatc tgacatgagt gcccgagcc gctccccctt	720
cgttctcgtc tcaataaata gtcattctc ttttatttgt tcatgtttca acagctgtct	780
agcgatcata tccgccatgc tgccatatcc aatcaatcca atctgttcca tcgactcagt	840
cctttcatat acaatatgaa gtgtaccggt ttccgcactt tttcacaatt tcccataatc	900
ttttcatttt tatcccacag tttttgttta tgataaaactc aagtcataaa cctatcaata	960

taaatagaca tgtgaaaata gagaaacgga gtgaacatg atg gat aac tat cgt	1014
Met Asp Asn Tyr Arg	
1 5	
gat gaa aac aga acg aaa ggt aat gag aat gag gtc ttt tta acg aaa	1062
Asp Glu Asn Arg Thr Lys Gly Asn Glu Asn Glu Val Phe Leu Thr Lys	
10 15 20	
gag aac gat cag agc gcc tcc tac tcg gcc cgc aat gtc att cat gat	1110
Glu Asn Asp Gln Ser Ala Ser Tyr Ser Ala Arg Asn Val Ile His Asp	
25 30 35	
cag gag aag aaa aaa cga gga ttc gga tgg ttc aga ccg ttg ctt ggc	1158
Gln Glu Lys Lys Arg Gly Phe Gly Trp Phe Arg Pro Leu Leu Gly	
40 45 50	
gga gtg atc ggc ggc agt ctt gct ctt ggc att tac acg ttt aca ccg	1206
Gly Val Ile Gly Gly Ser Leu Ala Leu Gly Ile Tyr Thr Phe Thr Pro	
55 60 65	
ctt ggt aac cat gat tct cag gac act gca aaa caa tca tcc agc cag	1254
Leu Gly Asn His Asp Ser Gln Asp Thr Ala Lys Gln Ser Ser Ser Gln	
70 75 80 85	
cag caa acg caa tct gtt aca gca aca agc acc tcc tct gaa tct aaa	1302
Gln Gln Thr Gln Ser Val Thr Ala Thr Ser Thr Ser Ser Glu Ser Lys	
90 95 100	
aaa agc tca agc agc tca tct gca ttc aag agc gag gac tct tct aaa	1350
Lys Ser Ser Ser Ser Ser Ser Ala Phe Lys Ser Glu Asp Ser Ser Lys	
105 110 115	
atc tca gat atg gta gaa gac ctt tca cca gcg att gtc ggt att aca	1398
Ile Ser Asp Met Val Glu Asp Leu Ser Pro Ala Ile Val Gly Ile Thr	
120 125 130	
aat ctt cag gca caa tca aac agc tct ttg ttc ggc tct agt tct tct	1446
Asn Leu Gln Ala Gln Ser Asn Ser Ser Leu Phe Gly Ser Ser Ser Ser	
135 140 145	
gat tcc agc gaa gat aca gaa agc ggt tca ggg tca ggt gtc att ttc	1494
Asp Ser Ser Glu Asp Thr Glu Ser Gly Ser Gly Ser Gly Val Ile Phe	
150 155 160 165	
aaa aaa gag aat ggc aag gct tat atc att aca aat aac cac gtc gta	1542
Lys Lys Glu Asn Gly Lys Ala Tyr Ile Ile Thr Asn Asn His Val Val	
170 175 180	
gaa ggg gca tca tca ctg aag gta tct tta tat gac ggc act gag gtt	1590
Glu Gly Ala Ser Ser Leu Lys Val Ser Leu Tyr Asp Gly Thr Glu Val	
185 190 195	
act gca aag ctg gta ggc agt gac tcg tta act gat tta gcc gtc ctc	1638
Thr Ala Lys Leu Val Gly Ser Asp Ser Leu Thr Asp Leu Ala Val Leu	
200 205 210	
caa atc agt gat gac cac gtc aca aaa gtg gca aac ttc ggt gat tca	1686
Gln Ile Ser Asp Asp His Val Thr Lys Val Ala Asn Phe Gly Asp Ser	

215	220	225	
tct gat ctt aga aca ggc gag acc gtt att gcg att ggg gat ccg ctt Ser Asp Leu Arg Thr Gly Glu Thr Val Ile Ala Ile Gly Asp Pro Leu 230 235 240 245			1734
gga aaa gac ctg tcc cgc aca gta aca caa gga att gta agc ggc gtg Gly Lys Asp Leu Ser Arg Thr Val Thr Gln Gly Ile Val Ser Gly Val 250 255 260			1782
gac aga acg gtt tca atg tct aca tca gcc ggc gaa acg agc att aac Asp Arg Thr Val Ser Met Ser Thr Ser Ala Gly Glu Thr Ser Ile Asn 265 270 275			1830
gtc att cag aca gac gca gca att aat cca ggt aac agc ggc ggt cct Val Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn Ser Gly Gly Pro 280 285 290			1878
ttg tta aat aca gac ggc aaa att gtc ggc att aac agt atg aaa atc Leu Leu Asn Thr Asp Gly Lys Ile Val Gly Ile Asn Ser Met Lys Ile 295 300 305			1926
agt gag gat gat gtt gag ggt atc gga ttc gcc att cca agc aat gac Ser Glu Asp Asp Val Glu Gly Ile Gly Phe Ala Ile Pro Ser Asn Asp 310 315 320 325			1974
gta aaa ccg att gct gaa gaa ttg ctg tct aaa gga caa att gaa cgt Val Lys Pro Ile Ala Glu Glu Leu Leu Ser Lys Gly Gln Ile Glu Arg 330 335 340			2022
cca tat atc ggt gtc agc atg ctt gat cta gag caa gtg ccg caa aat Pro Tyr Ile Gly Val Ser Met Leu Asp Leu Glu Gln Val Pro Gln Asn 345 350 355			2070
tac caa gaa ggc aca ctc ggc ctg ttc ggc agc cag ctg aat aaa ggc Tyr Gln Glu Gly Thr Leu Gly Leu Phe Gly Ser Gln Leu Asn Lys Gly 360 365 370			2118
gtt tac atc cgt gag gtc gct tca ggc tct cct gct gaa aag gcc gga Val Tyr Ile Arg Glu Val Ala Ser Gly Ser Pro Ala Glu Lys Ala Gly 375 380 385			2166
tta aaa gcg gag gat att atc atc ggc cta aaa ggt aaa gaa att gat Leu Lys Ala Glu Asp Ile Ile Ile Gly Leu Lys Gly Lys Glu Ile Asp 390 395 400 405			2214
aca ggc agt gaa ttg cgc aat atc tta tat aaa gac gca aag atc ggt Thr Gly Ser Glu Leu Arg Asn Ile Leu Tyr Lys Asp Ala Lys Ile Gly 410 415 420			2262
gat acc gtt gaa gtg aaa att ctc cga aac ggc aaa gaa atg acg aaa Asp Thr Val Glu Val Lys Ile Leu Arg Asn Gly Lys Glu Met Thr Lys 425 430 435			2310
aaa att aaa ctg gat caa aaa gaa gag aaa act tcg taa Lys Ile Lys Leu Asp Gln Lys Glu Glu Lys Thr Ser 440 445			2349

<210> 2
 <211> 449
 <212> PRT
 <213> *Bacillus subtilis*

<400> 2

Met Asp Asn Tyr Arg Asp Glu Asn Arg Thr Lys Gly Asn Glu Asn Glu
 1 5 10 15

Val Phe Leu Thr Lys Glu Asn Asp Gln Ser Ala Ser Tyr Ser Ala Arg
 20 25 30

Asn Val Ile His Asp Gln Glu Lys Lys Lys Arg Gly Phe Gly Trp Phe
 35 40 45

Arg Pro Leu Leu Gly Gly Val Ile Gly Gly Ser Leu Ala Leu Gly Ile
 50 55 60

Tyr Thr Phe Thr Pro Leu Gly Asn His Asp Ser Gln Asp Thr Ala Lys
 65 70 75 80

Gln Ser Ser Ser Gln Gln Thr Gln Ser Val Thr Ala Thr Ser Thr
 85 90 95

Ser Ser Glu Ser Lys Lys Ser Ser Ser Ser Ser Ser Ala Phe Lys Ser
 100 105 110

Glu Asp Ser Ser Lys Ile Ser Asp Met Val Glu Asp Leu Ser Pro Ala
 115 120 125

Ile Val Gly Ile Thr Asn Leu Gln Ala Gln Ser Asn Ser Ser Leu Phe
 130 135 140

Gly Ser Ser Ser Ser Asp Ser Ser Glu Asp Thr Glu Ser Gly Ser Gly
 145 150 155 160

Ser Gly Val Ile Phe Lys Lys Glu Asn Gly Lys Ala Tyr Ile Ile Thr
 165 170 175

Asn Asn His Val Val Glu Gly Ala Ser Ser Leu Lys Val Ser Leu Tyr
 180 185 190

Asp Gly Thr Glu Val Thr Ala Lys Leu Val Gly Ser Asp Ser Leu Thr
 195 200 205

Asp Leu Ala Val Leu Gln Ile Ser Asp Asp His Val Thr Lys Val Ala
 210 215 220

Asn Phe Gly Asp Ser Ser Asp Leu Arg Thr Gly Glu Thr Val Ile Ala
 225 230 235 240

Ile Gly Asp Pro Leu Gly Lys Asp Leu Ser Arg Thr Val Thr Gln Gly
 245 250 255

Ile Val Ser Gly Val Asp Arg Thr Val Ser Met Ser Thr Ser Ala Gly
 260 265 270

Glu Thr Ser Ile Asn Val Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly
 275 280 285

Asn Ser Gly Gly Pro Leu Leu Asn Thr Asp Gly Lys Ile Val Gly Ile
 290 295 300

Asn Ser Met Lys Ile Ser Glu Asp Asp Val Glu Gly Ile Gly Phe Ala
 305 310 315 320

Ile Pro Ser Asn Asp Val Lys Pro Ile Ala Glu Glu Leu Leu Ser Lys
 325 330 335

Gly Gln Ile Glu Arg Pro Tyr Ile Gly Val Ser Met Leu Asp Leu Glu
 340 345 350

Gln Val Pro Gln Asn Tyr Gln Glu Gly Thr Leu Gly Leu Phe Gly Ser
 355 360 365

Gln Leu Asn Lys Gly Val Tyr Ile Arg Glu Val Ala Ser Gly Ser Pro
 370 375 380

Ala Glu Lys Ala Gly Leu Lys Ala Glu Asp Ile Ile Ile Gly Leu Lys
 385 390 395 400

Gly Lys Glu Ile Asp Thr Gly Ser Glu Leu Arg Asn Ile Leu Tyr Lys
 405 410 415

Asp Ala Lys Ile Gly Asp Thr Val Glu Val Lys Ile Leu Arg Asn Gly
 420 425 430

Lys Glu Met Thr Lys Lys Ile Lys Leu Asp Gln Lys Glu Glu Lys Thr
 435 440 445

Ser

<210> 3
<211> 8
<212> DNA
<213> Artificial

<220>
<223> octameric motif

<220>
<221> octameric_motif
<222> (1)..(8)

<400> 3
ttttcata

8

<210> 4
<211> 44
<212> DNA
<213> Artificial

<220>
<223> Primer

<220>
<221> Primer_oth48
<222> (1)..(44)

<400> 4
gttcacgat cgcacggct aatcacacca ctcgggtga aggc

44

<210> 5
<211> 50
<212> DNA
<213> Artificial

<220>
<223> Primer

<220>
<221> Primer_oth50
<222> (1)..(50)

<400> 5
ggagcggatt gaacatgcga ttaaatatcc ttcgagacat ttccgatcgc

50

<210> 6
<211> 21
<212> DNA

<213> Artificial

<220>

<223> Primer

<220>

<221> Primer_260558

<222> (1) .. (21)

<400> 6

gagtatcgcc agtaaggggc g

21

<210> 7

<211> 44

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 7

gccttcaccc gaagtggctt gattagccga tgcgatcgat gaac

44

<210> 8

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Primer

<220>

<221> Primer_260559

<222> (1) .. (23)

<400> 8

gcagccctaa aatcgcataa agc

23

<210> 9

<211> 50

<212> DNA

<213> Artificial

<220>

<223> Primer

<220>

<221> Primer_oth51

<222> (1) .. (50)

<400> 9

gcgatcgaaa atgtctcgaa ggatatttaa tgcgatgttc aatccgctcc

50

<210> 10
<211> 28
<212> DNA
<213> Artificial

<220>
<223> Primer

<220>
<221> Primer_YKDA6
<222> (1)..(28)

<400> 10
gcgaattcta aactcaagtc ataaacct

28

<210> 11
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Primer

<220>
<221> Primer_YKDAP1
<222> (1)..(26)

<400> 11
gcggatccga tgatgaatga cattgc

26